

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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1 ATC TTTGTTTCTAGT TTACCTCAGG GCTATTATGA 33

34 AATGAAATGA GATAACCAAT GTGAAAGTCC TATAAACTGT ATAGCCTCCA TTCGGATGTA 93

94 TGTCTTTGGC AGGATGATAA AGAATCAGGA AGAAGGAGTA TCCACGTTAG CCAAGTGTCC 153

154 AGGCTGTGTC TGCTCTTATT TTAGTGACAG ATGTTGCTCC TGACAGAAGC TATTCTTCAG 213

214 GAAACATCAC ATCCAATATG GTAAATCCAT CAAACAGGAG CTAAGAAACA GGAATGAGAT 273

274 GGGCACTTGC CCAAGGAAAA ATGCCAGGAG AGCAAATAAT GATGAAAAAT AAACCTTTTCC 333

334 CTTTGTTTTT AATTTTCAGGA AAAAAATGATG AGGACCAAAA TCAATGAATA AGGAAAAACAG 393  
(Pr1.FPIII) CCTG AAAATGAATA AGAAA

394 CTCAGAAAAA AGATGTTTCC AAATTGGTAA TTAAGTATTT GTTCCTTGGG AAGAGACCTC 453  
(PR/GR-MMTV) T GTTCTTTTGG AA  
(SSRE) GAGACC

454 CATGTGAGCT TGATGGGAAA ATGGGAAAAA CGTCAAAAGC ATGATCTGAT CAGATCCCAA 513

514 AGTGGATTAT TATTTTAAAA ACCAGATGGC ATCACTCTGG GGAGGCAAGT TCAGGAAGGT 573

574 CATGTTAGCA AAGGACATAA CAATAACAGC AAAATCAAAA TTCCGCAAAT GCAGGAGGAA 633  
CCTTTTAG-A AAGGACAAAA CAGAATG (nGRE-PRL)

634 AATGGGGACT GGGAAAGCTT TCATAACAGT GATTAGGCAG TTGACCATGT TCGCAACACC 693

694 TCCCCGTCTA TACCAGGGAA CACAAAAATT GACTGGGCTA AGCCTGGACT TTCAAGGGAA 753  
GCCTGGACT GTC (CBE-P53)

754 ATATGAAAAA CTGAGAGCAA AACAAAAGAC ATGGTTAAAA GGCAACCAGA ACATTGTGAG 813  
ATTTTTCTGA TTGGTTAAAA GT (NFE1)

814 CCTTCAAAGC AGCAGTGCCC CTCAGCAGGG ACCCTGAGGC ATTTGCCTTT AGGAAGGCCA 873  
G ACCCTGAGGC T (KTF.1-CS)

874 GTTTTCTTAA GGAATCTTAA GAAACTCTTG AAAGATCATG AATTTTAACC ATTTTAAGTA 933

934 TAAAACAAAT ATGCGATGCA TAATCAGTTT AGACATGGGT CCCAATTTTA TAAAGTCAGG 993  
(PRE-lysozyme) AGGCCGT

994 CATACAAGGA TAACGTGTCC CAGCTCCGGA TAGGTCAGAA ATCATTAGAA ATCACTGTGT 1053  
GATCCAAGGA GCAGAAGTTC CAGCTATGGT CAG (GRE-hMT) GG TCACTGTGT

1054 CCCCATCCTA ACTTTTTTCAG AATGATCTGT CATAGCCCTC ACACACAGGC CCGATGTGTC 1113  
CCT

1114 TGACCTACAA CCACATCTAC AACCCAAGTG CCTCAACCAT TGTTAACGTG TCATCTCAGT 1173

**FIG. 1A**

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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1174 AGGTCCCATT ACAAATGCCA CCTCCCCTGT GCAGCCCATC CCGCTCCACA GGAAGTCTCC 1233

1234 CCACTCTAGA CTTCTGCATC ACGATGTTAC AGCCAGAAGC TCCGTGAGGG TGAGGGTCTG 1293  
(SSRE) GGTCTC

1294 TGTCTTACAC CTACCTGTAT GCTCTACACC TGAGCTCACT GCAACCTCTG CCTCCCAGGT 1353

1354 TCAAGCAATT CTCCTGTCTC AGCCTCCCGC GTAGCTGGGA CTACAGGCGC ACGCCCGGCT 1413  
C AGCCCCCGC GCAGC (ETF, EGFR)

1414 AATTTTGTGA TTGTTAGTAG AGATGGGGTT TCACCATATT AGCCCGGCTG GTCTTGAAGT 1473  
Alu Repeat Region CCATATT AGG (SRE-cFos)

1474 CCTGACCTCA GGTGATCCAC CCACCTCAGC CTCCTAAAGT GCTGGGATTA CAGGCATGAG 1533

1534 TCACCGCGCC CGGCCAAGGG TCAGTGTTTA ATAAGGAATA ACTTGAATGG TTTACTAAAC 1593

1594 CAACAGGGAA ACAGACAAAA GCTGTGATAA TTTCAGGGAT TCTTGGGATG GGAATGGTG 1653

1654 CCATGAGCTG CCTGCCTAGT CCCAGACCAC TGGTCCTCAT CACTTTCTTC CCTCATCCTC 1713

1714 ATTTTCAGGC TAAGTTACCA TTTTATTCAC CATGCTTTTG TGTAAGCCT CCACATCGTT 1773

1774 ACTGAAATAA GAGTATACAT AACTAGTTC CATTTGGGGC CATCTGTGTG TGTGTATAGG 1833  
GTTTACAT AAAC (VBP-vitel) GG

1834 GGAGGAGGGC ATACCCCAGA GACTCCTTGA AGCCCCGGC AGAGGTTTCC TCTCCAGCTG 1893  
GGAKGAGG (MaIT-CS)

1894 GGGGAGCCCT GCAAGCACCC GGGGTCTTGG GTGTCCTGAG CAACCTGCCA GCCCGTGCCA 1953

1954 CTGGTTGTTT TGTTATCACT CTCTAGGGAC CTGTTGCTTT CTATTTCTGT GTGACTCGTT 2013

2014 CATTCAATCA GGCATTCAAT GACAATTTAT TGAGTACTTA TATCTGCCAG ACACCAGAGA 2073

2074 CAAAATGGTG AGCAAAGCAG TCACTGCCCT ACCTTCGTGG AGGTGACAGT TTCTCATGGA 2133

2134 AGACGTGCAG AAGAAAATTA ATAGCCAGCC AACTTAAACC CAGTGCTGAA AGAAAGGAAA 2193  
GCGTGAC CGGAGCTGAA AGAAAGGAAC

2194 TAAACACCAT CTTGAAGAAT TGTGCGCAGC ATCCCTTAAC AAGGCCACCT CCCTAGCGCC 2253  
AC (ERE-c.vitel)

2254 CCCTGCTGCC TCCATCGTGC CCGGAGGCC CCAAGCCGA GTCTTCCAAG CCTCCTCCTC 2313

2314 CATCAGTCAC AGCGCTGCAG CTGGCCTGCC TCGCTTCCcG TGAATCGTCC TGGTGCATCT 2373  
AGCAG CTGGC (NF-mutagen)

2374 GAGCTGGAGA CTCCTTGGCT CCAGGCTCCA GAAAGGAAAT GGAGAGGGAA ACTAGTCTAA 2433  
A GAAAGGGAAA GGA (PRF-myc)

2434 CGGAGAATCT GGAGGGGACA GTGTTTCCTC AGAGGGAAAG GGGCCTCCAC GTCCAGGAGA 2493  
ACCCGGTACA CTGTGTCCTC CCGCT (GRE-hMT.IIa)  
CC CTTTGGGCCA ATGTGTCCTG AGGGGA (GRE-hGH)

FIG.1B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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2494 ATTCCAGGAG GTGGGGACTG CAGGGAGTGG GGACGCTGGG GCTGAGCGGG TGCTGAAAGG 2553  
CTGG GGAGCCTGGG GA (AP.2-SV40)

2554 CAGGAAGGTG AAAAGGGCAA GGCTGAAGCT GCCCAGATGT TCAGTGTTGT TCACGGGGCT 2613

2614 GGGAGTTTTT CGTTGCTTCC TGTGAGCCTT TTTATCTTTT CTCTGCTTGG AGGAGAAGAA 2673  
CT CGTTGCTTCG AG (HSTF-hsp70)

2674 GTCTATTTCA TGAAGGGATG CAGTTTCATA AAGTCAGCTG TTAATAATTCC AGGGTGTGCA 2733  
A

2734 TGGGTTTTCC TTCACGAAGG CCTTTATTTA ATGGGAATAT AGGAAGCGAG CTCATTTTCCT 2793  
TGGGTTTTTG (SBF.yeast)

2794 AGGCCGTTAA TTCACGAAG AAGTGAAGTGG AGTCTTTTCT TTCATGTCTT CTGGGCAACT 2853

2854 ACTCAGCCCT GTGGTGGACT TGGCTTATGC AAGACGGTCG AAAACCTTGG AATCAGGAGA 2913

2914 CTCGGTTTTT TTTCTGGTTC TGCCATTGGT TGGCTGTGCG ACCGTGGGCA AGTGTCTCTC 2973  
C TTTCTGGTTT TGCAG (NF.1-bithorax)  
(NF-MHCII/)/CCATTGGT T

2974 CTTCCCTGGG CCATAGTCTT CTCTGCTATA AAGACCCTTG CAGCTCTCGT GTTCTGTGAA 3033

3034 CACTTCCCTG TGATTCTCTG TGAGGGGGGA TGTGAGAGG GGAAGGAGGC AGAGCTGGAG 3093

3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGA CAGGAAGGCA GGCAGAAGCT GGGTGCTCCA 3153

3154 TCAGTCTCA CTGATCAGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943

2944 CAATGAACCC AACAGCCACA TTTTCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273

3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTTGCC TGGCATTCAA AAAGTGGGCC 3333  
GAAGTGACT AACTG (PEA.1-Polyoma)

3334 AGAGCAAGTG GAAAATGCCA GAGATTGTTA AACTTTTAC CCTGACCAGC ACCCCACGCA 3393

3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453  
C AGGTCAGAGT GACCTG (ERE.2-Vitel.)

3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCATTCA AGGGCAGTGG GAATTGACCA 3513

3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573  
(GRE-FLV) CGGGATAC CGAGAGAACA GGGCTATAGG

3574 AAAATCAGTT CAAGGGAAGT CGGGAGACCT GATTCTAAT ACTATATTTT TCCTTTACAA 3633  
GAGACC (SSRE)

3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGTA GTAAGTGG CTGTAAGATT ACTTAGTTTC 3693  
(ICS-MTII/ HLA-DR/ )AGTTTC

3694 TCCTTATTAG GAACTCTTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTTCTT 3753  
TCCTCT

3754 TTAACAGGAA GAAAACATTC CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813

3814 GACTATATGA TTGGTTTTTT GAAAAATCAT TTCAGCGATG TTTACTATCT GATTCAGAAA 3873

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FIG.1C

[illegible]

FIG. 1D







APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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3094 CAGCTGAGCC ACAGGGGAGG TGGAGGGGGA CAGGAAGGCA GGCAGAAGCT GGGTGCTCCA 3153  
3154 TCAGTCCTCA CTGATCACGT CAGACTCCAG GACCGAGAGC CACAATGCTT CAGGAAAGCT 2943  
2944 CAATGAACCC AACAGCCCACA TTTTCCTTCC CTAAGCATAG ACAATGGCAT TTGCCAATAA 3273  
3274 CCAAAAAGAA TGCAGAGACT AACTGGTGGT AGCTTTTGCC TGGCATTCAA AAAGTGGGCC 3333  
3334 AGAGCAAGTG GAAAATGCCA GAGATTGTGA AACTTTTCAC CCTGACCAGC ACCCCACGCA 3393  
3394 GCTCAGCAGT GACTGCTGAC AGCACGGAGT GACCTGCAGC GCAGGGGAGG AGAAGAAAAA 3453  
3454 GAGAGGGATA GTGTATGAGC AAGAAAGACA GATTCATTCA AGGGCAGTGG GAATTGACCA 3513  
3514 CAGGGATTAT AGTCCACGTG ATCCTGGGTT CTAGGAGGCA GGGCTATATT GTGGGGGGAA 3573  
3574 AAAATCAGTT CAAGGGAAGT CGGGAGACCT GATTTCTAAT ACTATATTTT TCCTTTACAA 3633  
3634 GCTGAGTAAT TCTGAGCAAG TCACAAGGTA GTAAGTGGG CTGTAAGATT ACTTAGTTTC 3693  
3694 TCCTTATTAG GAACTCTTTT TCTCTGTGGA GTTAGCAGCA CAAGGGCAAT CCCGTTTCTT 3753  
3754 TTAACAGGAA GAAAACATTC CTAAGAGTAA AGCCAAACAG ATTCAAGCCT AGGTCTTGCT 3813  
3814 GACTATATGA TTGGTTTTTT GAAAAATCAT TTCAGCGATG TTTACTATCT GATTGAGAAA 3873  
3874 ATGAGACTAG TACCCTTTGG TCAGCTGTAA ACAAACACCC ATTTGTAAAT GTCTCAAGTT 3933  
3934 CAGGCTTAAC TGCAGAACCA ATCAAATAAG AATAGAATCT TTAGAGCAAA CTGTGTTTCT 3993  
3994 CCACTCTGGA GGTGAGTCTG CCAGGGCAGT TTGGAAATAT TTAAGTTCACA AGTATTGACA 4053  
4054 CTGTTGTTGG TATTAACAAC ATAAAGTTGC TCAAAGGCAA TCATTATTTT AAGTGGCTTA 4113  
4114 AAGTTACTTC TGACAGTTTT GGTATATTTA TTGGCTATTG CCATTGCTT TTTGTTTTTT 4173  
4174 CTCTTTGGGT TTATTAATGT AAAGCAGGGA TTATTAACCT ACAGTCCAGA AAGCCTGTGA 4233  
4234 ATTTGAATGA GGAAAAAATT ACGTTTTTAT TTTTACCACC TTCTAACTAA ATTTAACATT 4293  
4294 TTATTCCATT GCGAATAGAG CCATAAACTC AAAGTGGTAA TAAGAGTACC TGTGATTTTG 4353  
4354 TCATTACCAA TAGAAATCAC AGACATTTTA TACTATATTA CAGTTGTTGC AGGTACGTTG 4413  
4414 TAAGTGAAAT ATTTATACTC AAACTACTT TGAAATTAGA CCTCCTGCTG GATCTTGTTT 4473  
4474 TTAACATATT AATAAAACAT GTTTAAAATT TTGATATTTT GATAATCATA TTTCATTATC 4533  
4534 ATTTGTTTCC TTTGTAATCT ATATTTTATA TATTTGAAAA CATCTTTCTG AGAAGAGTTC 4593  
4594 CCCAGATTTT ACCAATGAGG TTCTTGGCAT GCACACACAC AGAGTAAGAA CTGATTTAGA 4653  
4654 GGCTAACATT GACATTGGTG CCTGAGATGC AAGACTGAAA TTAGAAAGTT CTCCCAAAGA 4713

FIG.2C

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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4714 TACACAGTTG TTTTAAAGCT AGGGGTGAGG GGGGAAATCT GCCGCTTCTA TAGGAATGCT 4773  
4774 CTCCCTGGAG CCTGGTAGGG TGCTGTCCTT GTGTTCTGGC TGGCTGTTAT TTTTCTCTGT 4833  
4834 CCCTGCTACG TCTTAAAGGA CTTGTTTGGG TCTCCAGTTC CTAGCATAGT GCCTGGCACA 4893  
4894 GTGCAGGTTC TCAATGAGTT TGCAGAGTGA ATGGAAATAT AACTAGAAA TATATCTTTG 4953  
4954 TTGAAATCAG CACACCAGTA GTCCTGGTGT AAGTGTGTGT ACGTGTGTGTGTGT GTGTGTGTGT5017  
5018 GTGTGTGTGT AAAACCAGGT GGAGATATAG GAACTATTAT TGGGGTATGG GTGCATAAAT 5077  
5078 TGGGATGTTT TTTTAAAAA GAACTCCAA ACAGACTTCT GGAAGGTTAT TTTCTAAGAA 5137  
5138 TCTTGCTGGC AGCGTGAAGG CAACCCCTT GTGCACAGCC CCACCCAGCC TCACGTGGCC 5197  
5198 ACCTCTGTCT TCCCCATGA AGGGCTGGCT CCCAGTATA TATAAACCTC TCTGGAGCTC 5257  
5258 GGGCATGAGC CAGCAAGGCC ACCCATCCAG GCACCTCTCA GCACAGC 5304

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FIG.2D

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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1 ATCTTTGTTT AGTTTACCTC AGGGCTATTA TGAAATGAAA TGAGATAACC  
 51 AATGTGAAAG TCCTATAAAC TGTATAGCCT CCATTCCGAT GTATGTCTTT  
 101 GGCAGGATGA TAAAGAATCA GGAAGAAGGA GTATCCACGT TAGCCAAGTG  
 151 TCCAGGCTGT GTCTGCTCTT ATTTTAGTGA CAGATGTTGC TCCTGACAGA  
 201 AGCTATTCTT CAGGAAACAT CACATCCAAT ATGGTAAATC CATCAAACAG  
 251 GAGCTAAGAA ACAGGAATGA GATGGGCACT TGCCCAAGGA AAAATGCCAG  
 301 GAGAGCAAAT AATGATGAAA AATAAACTTT TCCCTTTGTT TTTAATTTCA  
 351 GGAAAAAATG ATGAGGACCA AAATCAATGA ATAAGGAAAA CAGCTCAGAA  
 401 AAAAGATGTT TCCAAATTGG TAATTAAGTA TTTGTTCTT GGAAGAGAC  
 451 CTCCATGTGA GCTTGATGGG AAAATGGGAA AAACGTCAAA AGCATGATCT  
 501 GATCAGATCC CAAAGTGGAT TATTATTTTA AAAACCAGAT GGCATCACTC  
 551 TGGGGAGGCA AGTTCAGGAA GGTGATGTTA GCAAAGGACA TAACAATAAC  
 601 AGCAAAATCA AAATTCCGCA AATGCAGGAG GAAAATGGGG ACTGGGAAAG  
 651 CTTTCATAAC AGTGATTAGG CAGTTGACCA TGTCGCAAC ACCTCCCCGT  
 701 CTATACCAGG GAACACAAAA ATTGACTGGG CTAAGCCTGG ACTTTCAAGG  
 751 GAAATATGAA AACTGAGAG CAAAACAAAA GACATGGTTA AAAGGCAACC  
 801 AGAACATTGT GAGCCTTCAA AGCAGCAGTG CCCCTCAGCA GGGACCCTGA  
 851 GGCATTTGCC TTTAGGAAGG CCAGTTTTCT TAAGGAATCT TAAGAACTC  
 901 TTGAAAGATC ATGAATTTTA ACCATTTTAA GTATAAAACA AATATGCGAT  
 951 GCATAATCAG TTTAGACATG GGTCCCAATT TTATAAAGTC AGGCATACAA  
 1001 GGATAACGTG TCCCAGCTCC GGATAGGTCA GAAATCATTG AATCACTG  
 1051 TGTCCCATC CTAACTTTTT CAGAATGATC TGTCATAGCC CTCACACACA  
 1101 GGCCCGATGT GTCTGACCTA CAACCACATC TACAACCCAA GTGCCTCAAC  
 1151 CATTGTTAAC GTGTCATCTC AGTAGGTCCC ATTACAAATG CCACCTCCCC  
 1201 TGTGCAGCCC ATCCCGCTCC ACAGGAAGTC TCCCACTCT AGACTTCTGC  
 1251 ATCACGATGT TACAGCCAGA AGCTCCGTGA GGGTGAGGGT CTGTGTCTTA

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FIG.3A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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1301 CACCTACCTG TATGCTCTAC ACCTGAGCTC ACTGCAACCT CTGCCTCCCA  
1351 GGTTCAGCA ATTCTCCTGT CTCAGCCTCC CGCGTAGCTG GGA CTACAGG  
1401 CGCACGCCCC GCTAATTTTT GTATTGTTAG TAGAGATGGG GTTTCACCAT  
1451 ATTAGCCCCG CTGGTCTTGA ACTCCTGACC TCAGGTGATC CACCCACCTC  
1501 AGCCTCCTAA AGTGCTGGGA TTACAGGCAT GAGTCACCGC GCGCGCCAA  
1551 GGGTCAGTGT TTAATAAGGA ATAAC TTGAA TGGTTTACTA AACCAACAGG  
1601 GAAACAGACA AAAGCTGTGA TAATTCAGG GATTCTTGGG ATGGGGAATG  
1651 GTGCCATGAG CTGCCTGCCT AGTCCCAGAC CACTGGTCCT CATCACTTTC  
1701 TTCCCTCATC CTCATTTTCA GGCTAAGTTA CCATTTTATT CACCATGCTT  
1751 TTGTGGTAAG CCTCCACATC GTTACTGAAA TAAGAGTATA CATAAACTAG  
1801 TTCCATTTGG GGCCATCTGT GTGTGTGTAT AGGGGAGGAG GGCATACCCC  
1851 AGAGACTCCT TGAAGCCCCC GGCAGAGGTT TCCTCTCCAG CTGGGGGAGC  
1901 CCTGCAAGCA CCCGGGGTCC TGGGTGTCCT GAGCAACCTG CCAGCCCGTG  
1951 CCACTGGTTG TTTTGTTATC ACTCTCTAGG GACCTGTTGC TTTCTATTTT  
2001 TGTGTGACTC GTTCATTCAT CCAGGCATTC ATTGACAATT TATTGAGTAC  
2051 TTATATCTGC CAGACACCAG AGACAAAATG GTGAGCAAAG CAGTCACTGC  
2101 CCTACCTTCG TGGAGGTGAC AGTTTCTCAT GGAAGACGTG CAGAAGAAAA  
2151 TTAATAGCCA GCCAACTTAA ACCCAGTGCT GAAAGAAAGG AAATAAACAC  
2201 CATCTTGAAG AATTGTGCGC AGCATCCCTT AACAAGGCCA CCTCCCTAGC  
2251 GCCCCCTGCT GCCTCCATCG TGCCCGGAGG CCCCCAAGCC CGAGTCTTCC  
2301 AAGCCTCCTC CTCCATCAGT CACAGCGCTG CAGCTGGCCT GCCTCGCTTC  
2351 CCGTGAATCG TCCTGGTGCA TCTGAGCTGG AGACTCCTTG GCTCCAGGCT  
2401 CCAGAAAGGA AATGGAGAGG GAAACTAGTC TAACGGAGAA TCTGGAGGGG  
2451 ACAGTGTTTC CTCAGAGGGA AAGGGGCCTC CACGTCCAGG AGAATTCCAG  
2501 GAGGTGGGGA CTGCAGGGAG TGGGGACGCT GGGGCTGAGC GGGTGCTGAA  
2551 AGGCAGGAAG GTGAAAAGGG CAAGGCTGAA GCTGCCCAGA TGTTCACTGT  
2601 TGTTACGGG GCTGGGAGTT TTCCGTTGCT TCCTGTGAGC CTTTTATCT

FIG.3B

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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4001 GGAGGTGAGT CTGCCAGGGC AGTTTGAAAA TATTTACTTC ACAAGTATTG  
4051 AACTGTTGT TGGTATTAAC AACATAAAGT TGCTCAAAGG CAATCATTAT  
4101 TTCAAGTGGC TTAAAGTTAC TTCTGACAGT TTTGGTATAT TTATTGGCTA  
4151 TTGCCATTTG CTTTTTGTTT TTTCTCTTTG GGTTTATTAA TGTAAGCAG  
4201 GGATTATTAA CCTACAGTCC AGAAAGCCTG TGAATTTGAA TGAGGAAAAA  
4251 ATTACATTTT TGTTTTTACC ACCTTCTAAC TAAATTTAAC ATTTTATTCC  
4301 ATTGCGAATA GAGCCATAAA CTCAAAGTGG TAATAACAGT ACCTGTGATT  
4351 TTGTCATTAC CAATAGAAAT CACAGACATT TTATACTATA TTACAGTTGT  
4401 TGCAGATACG TTGTAAGTGA AATATTTATA CTCAAAATA CTTTGAAATT  
4451 AGACCTCCTG CTGGATCTTG TTTTAAACAT ATTAATAAAA CATGTTTAAA  
4501 ATTTTGATAT TTTGATAATC ATATTTCAAT ATCATTTGTT TCCTTTGTAA  
4551 TCTATATTTT ATATATTTGA AAACATCTTT CTGAGAAGAG TTCCCCAGAT  
4601 TTCACCAATG AGGTTCTTGG CATGCACACA CACAGAGTAA GAACTGATTT  
4651 AGAGGCTAAC ATTGACATTG GTGCCTGAGA TGCAAGACTG AAATTAGAAA  
4701 GTTCTCCCAA AGATACACAG TTGTTTTAAA GCTAGGGGTG AGGGGGGAAA  
4751 TCTGCCGCTT CTATAGGAAT GCTCTCCCTG GAGCCTGGTA GGGTGCTGTC  
4801 CTTGTGTTCT GGCTGGCTGT TATTTTCTC TGTCCCTGCT ACGTCTTAAA  
4851 GGACTTGTTT GGATCTCCAG TTCCTAGCAT AGTGCCTGGC ACAGTGCAGG  
4901 TTCTCAATGA GTTTGCAGAG TGAATGGAAA TATAAACTAG AAATATATCC  
4951 TTGTTGAAAT CAGCACACCA GTAGTCCTGG TGTAAGTGTG TGTACGTGTG  
5001 TGTGTGTGTG TGTGTGTGTG TGTA AAAACCA GGTGGAGATA TAGGAACTAT  
5051 TATTGGGGTA TGGGTGCATA AATTGGGATG TTCTTTTTTAA AAAGAACTC  
5101 CAAACAGACT TCTGGAAGGT TATTTTCTAA GAATCTTGCT GGCAGCGTGA  
5151 AGGCAACCCC CCTGTGCACA GCCCCACCCA GCCTCACGTG GCCACCTCTG  
5201 TCTTCCCCCA TGAAGGGCTG GCTCCCCAGT ATATATAAAC CTCTCTGGAG  
5251 CTCGGGCATG AGCCAGCAAG GCCACCCATC CAGGCACCTC TCAGCACAGC 5300

FIG. 3D

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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1 AGAGCTTTCCAGAGGAAGCCTACCAAGCCTCTGCAATGAGGTTCTTCTGTGCACGTTGC 60  
61 TGCAGCTTTGGGCTGAGATGCCAGCTGTCCAGCTGCTGCTTCTGGCCTGCCTGGTGTGG 120  
121 GATGTGGGGGCCAGGACAGCTCAGCTCAGGAAGGCCAATGACCAGAGTGGCCGATGCCAG 180  
181 TATACCTTCAGTGTGGCCAGTCCCAATGAATCCAGCTGCCCAGAGCAGAGCCAGGCCATG 240  
241 TCAGTCATCCATAACTTACAGAGAGACAGCAGCACCCAACGCTTAGACCTGGAGGCCACC 300  
301 AAAGCTCGACTCAGCTCCCTGGAGAGCCTCCTCCACCAATTGACCTTGGACCAGGCTGCC 360  
361 AGGCCCCAGGAGACCCAGGAGGGGCTGCAGAGGGAGCTGGGCACCCTGAGGCGGGAGCGG 420  
421 GACCAGCTGGAACCCAAACCAGAGAGTTGGAGACTGCCTACAGCAACCTCCTCCGAGAC 480  
481 AAGTCAGTTCTGGAGGAAGAGAAGAAGCGACTAAGGCAAGAAAATGAGAATCTGGCCAGG 540  
541 AGGTTGGAAGCAGCAGCCAGGAGGTAGCAAGGCTGAGAAGGGGCCAGTGTCCCCAGACC 600  
601 CGAGACACTGCTCGGGCTGTGCCACCAGGCTCCAGAGAAG

(intron #1) gtaagaatgcagagtggggggactct  
gagttcagcaggtgatatggctcgtagtacgtgctacaggcgtccaggcctccctgcccctttctccta  
gagactgcacagctagcacaagacagatgaattaaggaaagcacacgatcaccttcaagtattacta  
gtaatttagctcctgagagcttcatttagattagtggttcagagttcttgtgccccctccatgtcag-----  
----- Intron I ~10 Kb-----  
aaggtaggcacattgccctgcaatttataatttatgaggtgttcaattatggaattgtcaaatattaaca  
aaagtagagagactacaatgaactccaatgtagccataactcaggcccaactgttatcagcacagtcc  
aatcatgttttatctttccttctctgaccccaacccatccccagtccttatctaaaatcaaatatcaaaca  
ccatactcttgggagcctatttatattagttagtttagtttcagacagagtttctttctgttcccaagctgg  
agtacaatagtgtagtcctcggtacacagcaatctccccctccttggttcaagcaattctectgcctcagtc  
tcccaagaagctgggattatagacacctgccaccacatccagctaattttttgtgttttagaaaagaca  
gggtttcaccatgttgccaggctgggttcgaactcctgacctcaggtgatccgcctgcctcgccctccca  
aagtgtgggattacaggcatgagccaccagcctggccggcagcctatttaaattgtcatcctcaacat  
agtcaatccttgggccattttttcttacagtaaaattttgtctctttcttttaacatcag

(exon #2) TT TCT ACG TGG AAT TTG GAC

661 ACT TTG GCC TTC CAG GAACTG AAG TCC GAG CTA ACT GAAGTTCTT GCT TCC CGA ATT TTG 720  
721 AAG GAG AGC CCA TCT GGCTAT CTC AGG AGT GGAGAG GGA GAC ACCG

(intron #2)  
gtatgaagttaagtttcttcccttttgtgcccacgtggtctttattcatgtctagtgtgttcagagaa  
tcagtatagggtaaatgccacccaagggggaaattaacttccctgggagcagagggagggaggga  
gaagaggaacagaactctctctctctctgttacccttgt----- Intron II ~ 3 kb-----

FIG.3E

002254 0100



2161 TTA AAG GTG TGT GTG TGT GTG TGT GTG TAA CTG AGA GGC TTG TGC CTG GTT TTG 2220

2221 AGG TGC TGC CCA GGA TGA CGC CAA GCA AAT AGC GCA TCC ACA CTT TCC CAC CTC CAT CTC 2280

2281 CTG GTG CTC TCG GCA CTA CCG GAG CAA TCT TTC CAT CTC TCC CCT GAA CCC ACC CTC TAT 2340

2341 TCA CCC TAA CTC CAC TTC AGT TTG CTT TTG ATT TTT TTT TTT TTT TTT TGA 2400

2401 GAT GGG GTC TCG CTC TGT CAC CCA GGC TGG AGT GCA GTG GCA CGA TCT CGG CTC ACT GCA 2460

2461 AGT TCC GCC TCC CAG GTT CAC ACC ATT CTC CTG CCT CAG CCT CCC AAG TAG CTG GGA CTA 2520

2521 CAG GCA CCT GCC ACC ACG CCT GGC TAA TTT TTT TTT TTT CCA GTG AAG ATG GGT TTC ACC 2580

2581 ATG TTA GCC AGG ATG GTC TCG ATC TCC TGAC CTT GTC ATC CAC CCA CCT TGG CCT CCC AAA 2640

2641 GTG CTG GGA TTA CAG GCG TGA GCC ACC ACGC CCA GCC CCT CCA CTT CAG TTT TTA TCT GTC 2700

2701 ATC AGG GGT ATG AAT TTT ATA AGC CAC ACC TCA GGT GGA GAA AGC TTG ATG CAT AGC TTG 2760

2761 AGT ATT CTA TAC TGT 2776

**FIG. 3G**



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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05710-1332250

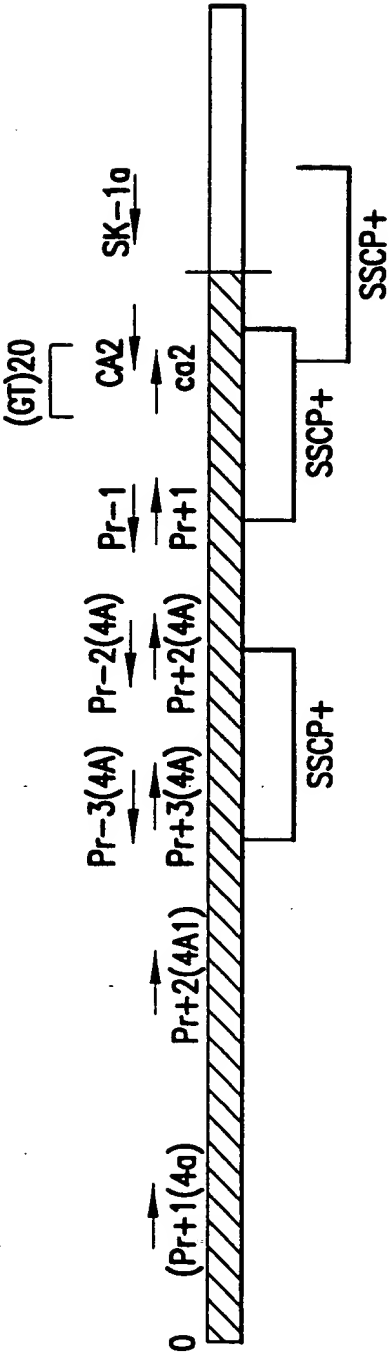


FIG.4

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

18/23

05TFO:TBZ2200

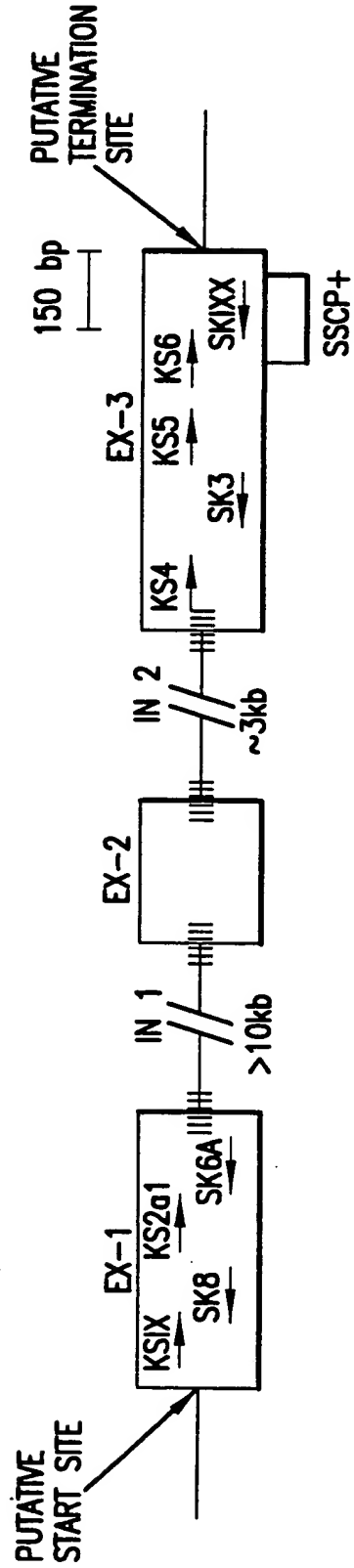


FIG.5

06 FEB 1980

TIGR	-TGAVVYSGS	LYFQGAESRT	VIRVELNTET	VKAKEIPGA	GYHGQFPYSW	GGYTDIDLAV	59
ym08h12.r1	-----	-----	--RFDLKTET	ILKTRSLDYA	GYNMNYHYAW	GGHSDIDLW	38
1B426bAMZ	GTGQVVYNGS	IYFNKFQSHI	IIRFDLKTET	ILKTRSLDYA	GYNMNYHYAW	GGHSDIDLW	60
ranofm	GAGVVHNNN	LYNCFNSHD	MCRASL-TSG	VYQKKPLLNA	LFNNRFSYAG	TMFQDMDFSS	59
Consensus	.G.VV....	.Y.....S...	.R..L.TET	.....L..A	GYN...YAW	GG..DIDL.V	60
TIGR	DEAGLWVIYS	TDEAKGAIVL	SKLNPENLEL	EQTWETNIRK	QSVANAFIIC	GTLYTVSSYT	119
ym08h12.r1	DESGLWAVYA	TNQAGNIVV	SRLDPVSLQT	LQTWNTSYPK	RXPGXAFIIC	GTCYVTNGY-	97
1B426bAMZ	DENGLWAVYA	TNQAGNIVI	SKLDPVSLQI	LQTWNTSYPK	RSAGEAFIIC	GTLYVTNGYS	120
ranofm	DEKGLWVIFT	TEKSAGKIVV	GKVNVAFTV	DNIWITTQNK	SDASNAFMIC	GVLVYVTRSLG	119
Consensus	DE.GLW..Y.	T...AG.IV.	SKL.P..L...	.QTW.T...K	....AFIIC	GTLYVT..Y.	120
TIGR	SADATVNFAY	DTGTGISKTL	TIPFKNRYKY	SSMIDYNPLE	KKLFANDNLN	MVTYDIKLS	178
ym08h12.r1	SGGTVVHYAY	QTNAST----	-----YEY	---IDI-PFQ	NKLP-----	--HFPC---	131
1B426bAMZ	GG-TKVHYAY	QTNASTYEYI	DIPFQNKYSH	ISMLDYNPKD	RALYANNNGH	QTLYNVTLF	178
ranofm	PKMEEVFYMF	DTKTGKEGHL	SIMMEKMAEK	VHLSYNSND	RKLYMFSEGY	LLHYDIAL-	177
Consensus	.....V.YAY	.T.....	.I.....Y..	....DYNP..	.KL.....	...Y...L.	178

FIG.6

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

66770-1352250

20/23

1 AGA GCT TTC CAG AGG AAG CCT CAC CAA GCC TCT GCA ATG AGG TTC TGT GCA CGT TGC 60  
 61 TGC AGC TTT GGG CCT GAG ATG CCA GCT GTC CAG CTG CTT CTG GCC TGC CTG GTG TGG 120  
 121 GAT GTG GGG GCC AGG ACA GCT CAG CTC AGG AAG GCC AAT GAC CAG AGT GGC CGA TGC CAG 180  
 181 TAT ACC TTC AGT GTG GCC AGT CCC AAT GAA TCC AGC TGC CCA GAG CAG AGC CAG GCC ATG 240  
 241 TCA GTC ATC CAT AAC TTA CAG AGA GAC AGC AGC ACC CAA CGC TTA GAC CTG GAG GCC ACC 300  
 301 AAA GCT CGA CTC AGC TCC CTG GAG AGC CTC CAC CAA TTG ACC TTG GAC CAG GCT GCC 360  
 361 AGG CCC CAG GAG ACC CAG GAG GGG CTG CAG AGG GAG CTG GGC ACC CTG AGG CGG GAG CGG 420  
 421 GAC CAG CTG GAA ACC CAA ACC AGA GAG TTG GAG ACT GCC TAC AGC AAC CTC CTC CGA GAC 480  
 481 AAG TCA GTT CTG GAG GAA GAG AAG AAG CGA CTA AGG CAA GAA AAT GAG AAT CTG GCC AGG 540  
 541 AGG TTG GAA AGC AGC CAG GAG GTA GCA AGG CTG AGA AGG GGC CAG TGT CCC CAG ACC 600  
 601 CGA GAC ACT GCT CGG GCT GTG CCA CCA GGC TCC AGA GAA GTT TCT ACG TGG AAT TTG GAC 660  
 661 ACT TTG GCC TTC CAG GAA CTG AAG TCC GAG CTA ACT GAA GTT CCT GCT TCC CGA ATT TTG 720  
 721 AAG GAG AGC CCA TCT GGC TAT CTC AGG AGT GGA GAG GGA GAC ACC GGA TGT GGA GAA CTA 780  
 781 GTT TGG GTA GGA GAG CCT CTC ACG CTG AGA ACA GCA GAA ACA ATT ACT GGC AAG TAT GGT 840  
 841 GTG TGG ATG CGA GAC CCC AAG CCC ACC TAC CCC TAC ACC CAG GAG ACC ACG TGG AGA ATC 900

FIG.7A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

21/23

66770-7332200

901 GAC ACA GTT GGC ACG GAT GTC CGC CAG GTT TTT GAG TAT GAC CTC ATC AGC CAG TTT ATG 960  
 961 CAG GGC TAC CCT TCT AAG GTT CAC ATA CTG CCT AGG CCA CTG GAA AGC ACG GGT GCT GTG 1020  
 1021 GTG TAC TCG GGG AGC CTC TAT TTC CAG GGC GCT GAG TCC AGA ACT GTC ATA AGA TAT GAG 1080  
 1081 CTG AAT ACC GAG ACA GTG AAG GCT GAG AAG GAA ATC CCT GGA GCT GGC TAC CAC GGA CAG 1140  
 1141 TTC CCG TAT TCT TGG GGT GGC TAC ACG GAC ATT GAC TTG GCT GTG GAT GAA GCA GGC CTC 1200  
 1201 TGG GTC ATT TAC AGC ACC GAT GAG GCC AAA GGT GCC ATT GTC CTC TCC AAA CTG AAC CCA 1260  
 1261 GAG AAT CTG GAA CTC GAA CAA ACC TGG GAG ACA AAC ATC CGT AAG CAG TCA GTC GCC AAT 1320  
 1321 GCC TTC ATC ATC TGT GGC ACC TTG TAC ACC GTC AGC AGC TAC ACC TCA GCA GAT GCT ACC 1380  
 1381 GTC AAC TTT GCT TAT GAC ACA GGC ACA GGT ATC AGC AAG ACC CTG ACC ATC CCA TTC AAG 1440  
 1441 AAC CGC TAT AAG TAC AGC AGC ATG ATT GAC TAC AAC CCC CTG GAG AAG AAG CTC TTT GCC 1500  
 1501 TGG GAC AAC TTG AAC ATG GTC ACT TAT GAC ATC AAG CTC TCC AAG ATG 1548

FIG.7B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

22/23

05710-7882260

1 Met Arg Phe Phe Cys Ala Arg Cys 20

21 Cys Ser Phe Gly Pro Glu Met Pro Ala Val Gln Leu Leu Leu Ala Cys Leu Val Trp 40

41 Asp Val Gly Ala Arg Thr Ala Gln Leu Arg Lys Ala Asn Asp Gln Ser Gly Arg Cys Gln 60

61 Tyr Thr Phe Ser Val Ala Ser Pro Asn Glu Ser Ser Cys Pro Glu Gln Ser Gln Ala Met 80

81 Ser Val Ile His Asn Leu Gln Arg Asp Ser Ser Thr Gln Arg Leu Asp Leu Glu Ala Thr 100

101 Lys Ala Arg Leu Ser Ser Leu Glu Ser Leu Leu His Gln Leu Thr Leu Asp Gln Ala Ala 120

121 Arg Pro Gln Glu Thr Gln Glu Gly Leu Gln Arg Glu Leu Gly Thr Leu Arg Arg Glu Arg 140

141 Asp Gln Leu Glu Thr Gln Thr Arg Glu Leu Glu Thr Ala Tyr Ser Asn Leu Leu Arg Asp 160

161 Lys Ser Val Leu Glu Glu Lys Lys Arg Leu Arg Gln Glu Asn Glu Asn Leu Ala Arg 180

181 Arg Leu Glu Ser Ser Gln Glu Val Ala Arg Leu Arg Arg Gly Gln Cys Pro gln Thr 200

201 Arg Asp Thr Ala Arg Ala Val Pro Pro Gly Ser Arg Glu Val Ser Thr Trp Asn Leu Asp 220

221 Thr Leu Ala Phe Gln Glu Leu Lys Ser Glu Leu Thr Glu Val Pro Ala Ser Arg Ile Leu 240

241 Lys Glu Ser Pro Ser Gly Tyr Leu Arg Ser Gly Glu Gly Asp Thr Gly Cys Gly Glu Leu 260

261 Val Trp Val Gly Glu Pro Leu Thr Leu Arg Thr Ala Glu Thr Ile Thr Gly Lys Tyr Gly 280

281 Val Trp Met Arg Asp Pro Lys Pro Thr Tyr Pro Tyr Thr Gln Glu Thr Thr Trp Arg Ile 300

FIG.8A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

00TFO-78842260

23/23

301 Asp Thr Val Gly Thr Asp Val Arg Gln Val Phe Glu Tyr Asp Leu Ile Ser Gln Phe Met 320  
 321 Gln Gly Tyr Pro Ser Lys Val His Ile Leu Pro Arg Pro Leu Glu Ser Thr Gly Ala Val 340  
 341 Val Tyr Ser Gly Ser Leu Tyr Phe Gln Gly Ala Glu Ser Arg Thr Val Ile Arg Tyr Glu 360  
 361 Leu Asn Thr Glu Thr Val Lys Ala Glu Lys Glu Ile Pro Gly Ala Gly Tyr His Gly Gln 380  
 381 Phe Pro Tyr Ser Trp Gly Gly Tyr Thr Asp Ile Asp Leu Ala Val Asp Glu Ala Gly Leu 400  
 401 Trp Val Ile Tyr Ser Thr Asp Glu Ala Lys Gly Ala Ile Val Leu Ser Lys Leu Asn Pro 420  
 421 Glu Asn Leu Glu Leu Glu Gln Thr Trp Glu Thr Asn Ile Arg Lys Gln Ser Val Ala Asn 440  
 441 Ala Phe Ile Ile Cys Gly Thr Leu Tyr Thr Val Ser Ser Tyr Thr Ser Ala Asp Ala Thr 460  
 461 Val Asn Phe Ala Tyr Asp Thr Gly Thr Gly Ile Ser Lys Thr Leu Thr Ile Pro Phe Lys 480  
 481 Asn Arg Tyr Lys Tyr Ser Ser Met Ile Asp Tyr Asn Pro Leu Glu Lys Lys Leu Phe Ala 500  
 501 Trp Asp Asn Leu Asn Met Val Thr Tyr Asp Ile Lys Leu Ser Lys Met

FIG.8B